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Aug 28 1999

TECH CENTER 1630 2900

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/214,913

DATE: 1999-08-11

TIME: 14:44:13

Input File: A:\88362112.app

Output File: N:\CRF3\08222001\I214913.raw

3 <110> APPLICANT: Smith, Richard  
 4 Dodd, Ian  
 5 Mossakowska, Danuta, Ewa, Irene  
 7 <120> TITLE OF INVENTION: COMBINATION OF POLYMER REPTILES COMBINED WITH  
 8 MEMBRANE-BINDING AGENTS  
 11 <130> FILE REFERENCE: 088362/0112  
 12 <140> CURRENT APPLICATION NUMBER: 09/214,913  
 13 <141> CURRENT FILING DATE: 1999-03-10  
 14 <150> PRIOR APPLICATION NUMBER: 2206255  
 15 <151> PRIOR FILING DATE: 1997-07-08  
 16 <150> PRIOR APPLICATION NUMBER: 9614871.3  
 17 <151> PRIOR FILING DATE: 1996-07-19  
 21 <160> NUMBER OF SEQ ID NOS: 51  
 23 <170> SOFTWARE: PatentIn Ver. 2.1  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 37  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: Artificial Sequence  
 30 <220> FEATURE:  
 31 <221> OTHER INFORMATION: Description of Artificial Sequence:  
 32 Oligonucleotide used to anneal to oligonucleotide  
 33 of SEQ ID NO.2  
 35 <400> SEQUENCE: 1  
 36 ggaacggaat gcatcatccc gaacaaatgc taataaa 37  
 38 <210> SEQ ID NO: 2  
 39 <211> LENGTH: 37  
 40 <212> TYPE: DNA  
 41 <213> ORGANISM: Artificial Sequence  
 43 <220> FEATURE:  
 44 <221> OTHER INFORMATION: Description of Artificial Sequence:  
 45 Oligonucleotide used to anneal to oligonucleotide  
 46 of SEQ ID NO.1  
 48 <400> SEQUENCE: 1  
 49 ggaacggaat gcatcatccc gaacaaatgc taataaa 37  
 51 <210> SEQ ID NO: 3  
 52 <211> LENGTH: 37  
 53 <212> TYPE: DNA  
 54 <213> ORGANISM: Artificial Sequence  
 56 <220> FEATURE:  
 57 <221> OTHER INFORMATION: Description of Artificial Sequence:  
 58 Oligonucleotide used to anneal to oligonucleotide  
 59 of SEQ ID NO.4  
 61 <400> SEQUENCE: 1  
 62 ggaacggaat gcatcatccc gaacaaatgc taataaa 37

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## RAW SEQUENCE LISTING

PATENT APPLICATION NO: US/09/214,913

DATE: 08/11/2009

TIME: 10:44:12

Input File: A:\88362112.app

Output File: N:\CRF3\08222001\I214913.raw

```

136 Phe His Thr Leu Ile Asn Gly Asp Ile Leu Ser Ile Asn Arg Ile Asn
137      138      139      140
139 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Tyr Asn Ile Gly Ser Gly
140 145      146      147      148
142 Gly Arg Lys Val Ile Glu Leu Val Gly Ser Ile Ser Ile Tyr Cys Thr
143      144      145      146
145 Ser Asn Asp Asp Gln Val Gly Ile Thr Ser Gly Ile Ala Ile Gln Cys
146      147      148      149
148 Ile Ile Pro Asn Lys Cys
149      150
152 <210> SEQ ID NO: 1
153 <211> LENGTH: 214
154 <212> TYPE: prt
155 <213> ORGANISM: Artificial Sequence
157 <220> FEATURE:
158 <223> OTHER INFORMATION: Description of Artificial Sequence: Short
159      consensus repeats 1-3 of CRI with an additional 17
160      C-terminal amino acids
162 <400> SEQUENCE: 1
163 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
164      1      5      10      15
165 Leu Thr Asp Glu Phe Glu Ile Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
166      20      25      30
167 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
168      35      40      45
169 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
170      50      55      60
171 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
172      65      70      75      80
173 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
174      85      90      95
175 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
176      100      105      110
177 Ile Trp Asp Asn Gln Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
178      115      120      125
179 Phe His Thr Leu Ile Asn Gly Asp Ile Leu Ser Ile Asn Arg Ile Asn
180      130      135      140
181 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Tyr Asn Ile Gly Ser Gly
182      145      150      155
183 Gly Arg Lys Val Ile Glu Leu Val Gly Ser Ile Ser Ile Tyr Cys Thr
184      160      165      170
185 Ser Asn Asp Asp Gln Val Gly Ile Thr Ser Gly Ile Ala Ile Gln Cys
186      175      180      185
187 Ile Ile Pro Asn Lys Asp Gly Ile Lys Lys Lys Lys Lys Lys Ser Ile
188      190      195      200
189 Ser Lys Ser Ser Gly Cys

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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/214,913

DATE: 09/11/2001

TIME: 10:44:11

Input File: A:\88362112.app

Output File: N:\CRF3\08222001\I214913.raw

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100 <213> ORGANISM: Artificial Sequence
111 <220> FEATURE:
112 <221> NAME/KEY: UNDEF
113 <222> LOCATION: (1..149)
114 <223> OTHER INFORMATION: Positions 1-149 are a short polypeptide chain and
115 residues 149-151 are a short polypeptide chain
116 linked by a disulfide bond formed between the
117 cysteines at positions 149 and 151
118 <220> FEATURE:
119 <221> NAME/KEY: UNDEF
121 <222> LOCATION: (151)
122 <223> OTHER INFORMATION: The C-terminal glycine is linked to an
123 N (Myristoyl) group
125 <220> FEATURE:
126 <221> NAME/KEY: UNDEF
127 <222> LOCATION: (198)
128 <223> OTHER INFORMATION: The cysteine at position 198 is -Cys-CONH
130 <220> FEATURE:
131 <221> NAME/KEY: UNDEF
132 <222> LOCATION: (149)
133 <223> OTHER INFORMATION: The cysteine at position 149 is CONH2-Cys-
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence:
137 [SCF1-3]-Cys-3'-[MSWP-1]
138 <400> SEQUENCE:
140 Met Gln Cys Asn Ala Ile Glu Trp Leu Ile Phe Ala Arg Pro Thr Asn
141 1 10 20 30 40 50 60 70 80 90 100 110 120 130 140 150
143 Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
144 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300
146 Cys Arg Ile Gly Tyr Ser Gly Arg Ile Phe Ser Ile Ile Cys Leu Lys
147 310 320 330 340 350 360 370 380 390 400 410 420 430 440 450
149 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Tyr Arg Arg Lys Ser Tyr
150 460 470 480 490 500 510 520 530 540 550 560 570 580 590 600
153 Arg Asn Ile Ile Asp Ile Val Asn Arg Met Thr His Val Thr Lys Gly
154 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750
156 Ile Val Ile Val Val Val Val Val Val Val Val Val Val Val Val Val Val
157 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900
159 Ile Thr Arg Asn Ala Thr Ile Ile Tyr Arg Arg Ile Ile Tyr Arg Ile
160 910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050
162 Pro Pro Thr Ile Ile Asn Gly Asp Ile Ile Ser Thr Asn Arg Ile Asn
163 1060 1070 1080 1090 1100 1110 1120 1130 1140 1150 1160 1170 1180 1190 1200
165 Ile His Thr Val Val Val Val Val Val Val Val Val Val Val Val Val Val
166 1210 1220 1230 1240 1250 1260 1270 1280 1290 1300 1310 1320 1330 1340 1350
168 149

```

## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/214,913

Figure 1. Schematic representation of the experimental design. The subjects were divided into two groups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group. The control group was divided into two subgroups: the control group and the experimental group. The experimental group was divided into two subgroups: the control group and the experimental group.

TABLE 1. *Continued*

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File Name      : A:\88362112.app

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N:\CRF3\08222001\I214913.raw

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276 Ile Ile Pro Asn Lys Lys Lys Asp Lys Ile Lys Lys Lys Lys Lys Lys
277      196      200      207
279 Ser Pro Ser Lys Ser Ser Gly
280      210      217
283 <210> FEATURE:
284 <211> LENGTH: 11
285 <212> TYPE: PKT
286 <213> ORGANISM: Artificial Sequence
288 <220> FEATURE:
289 <221> NAME/KEY: UNSURE
290 <222> LOCATION: (214)..(215)
291 <223> OTHER INFORMATION: Residues 1-214 are a first polypeptide chain and
292      215-217 are a second polypeptide chain
293      linked by a disulphide bond formed between the
294      cysteines at positions 214 and 215
296 <220> FEATURE:
297 <221> NAME/KEY: UNSURE
298 <222> LOCATION: (232)
299 <223> OTHER INFORMATION: The C-terminal lysine is linked to an
300      N-[Myristoyl] group
302 <220> FEATURE:
303 <223> OTHER INFORMATION: Description: Pi Artificial Sequence: [SCR1-3/switch
304      fusion] disulphide linked to [PCW1-1]
306 <220> FEATURE:
307 <221> NAME/KEY: UNSURE
308 <222> LOCATION: (214)
309 <223> OTHER INFORMATION: The cysteine at position 214 is -Cys-COOH
311 <220> FEATURE:
312 <221> NAME/KEY: UNSURE
313 <222> LOCATION: (211)
314 <223> OTHER INFORMATION: The cysteine at position 211 is -CONH2-Cys-
316 <400> SEQUENCE:
317 Met Gln Cys Asn Ala Ile Gln Trp Leu Phe Ile Ala Arg Phe Thr Asn
318      1      20      39      58      77      96      115      134
319 Leu Ile Arg Val Thr Ser Thr Ser Ile Val Ile Thr Ser Ser Asn Lys Val
320      153      172      191      210      229      248      267      286
321 Pro Asn Phe Val Ser Val Val Val Val Val Val Val Val Val Val Val
322      305      324      343      362      381      400
323 Asn Ser Val Thr Val Val Val Val Val Val Val Val Val Val Val Val
324      438      457      476      495      514      533      552      571
325 Arg Asn Leu Ile Arg Ile Val Asn Gly Met Val His Val Ile Lys Gly
326      609      628      647      666      685      704      723      742
327 Ile Ile Ile Lys Ser Ile Ile Ile Ile Lys Ser Ile Ile Lys Lys Lys Arg
328      780      800      819      838      857      876      895      914
329 Leu Ile Lys Gly Ser Ser Ser Asn Ile Lys Ile Ile Ser Lys Arg Thr Val

```

VERIFICATION SUMMARY

PATENT APPLICATION N: US/09/214,913

DATE: 11/11/2009

TIME: 11:44:11

Input File : A:\88362112.app

Output File : N:\CRF3\08222001\I214913.raw

## STATISTICS SUMMARY

PATENT APPLICATION: US/09/214,913

DATE: 09/11/2009

TIME: 11:44:11

Input File: A:\88362112.app

Input File: N:\CRF3\08222001\I214913.raw

Application Serial Number: 08222001, 214,913

Alpha: Numeric: Numeric

Application Class:

Application File Date: 09-11-2009

Alt Title:

Software Application: Patent

Total Number of Sequences: 11

Total Nucleotides: 114

Total Amino Acids: 187

Number of Errors: 0

Number of Warnings: 0

Number of Corrections: 0

## MESSAGE SUMMARY